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RAW SEQUENCE LISTING PATENT APPLICATION US/09/289,180

DATE: 06/15/1999
TIME: 14:20:18

Input Set: I289180.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1 <110> SHIMOKAWATOKO, Yasutaka
2 NISHIO, Shoichi
3 <120> A method for evaluating the ability of a compound to inhibit the protoporphyr
4 <130> 2185-324P
5 <140> US/09/289,180
6 <141> 1999-04-09
7 <150> JP 10/099619
8 <151> 1998-04-10
9 <160> 14

ERRORED SEQUENCES FOLLOW

	10	<210> 2	
	11	<211> 1638	
	12	<212> DNA	
	13	<213> Rattus norvegicus	
	14	<220>	
	15	<222> (143)...(1576)	
E-->	16	<400> ①2	
W-->	17	cgtaacgcgc cgttttgcac tagttgctca ttaatcagta agtgcccaga ggtgggggtac	60
W-->	18	gggacccgtg gggtttctgc agttgtaaag cagggtgcct cccgttctcc tggggatatct	120
W-->	19	cgactttccc ccaggcctta cg atg gcc cgg act gtg ata gtg ctt ggc gga	172
	20	Met Ala Arg Thr Val Ile Val Leu Gly Gly	
	21	1 5 10	
W-->	22	ggt atc agc gga ttg gcc gca agt tat cat ctg acc cga agc ccc agt	220
	23	Gly Ile Ser Gly Leu Ala Ala Ser Tyr His Leu Thr Arg Ser Pro Ser	
	24	15 20 25	
W-->	25	cct cct aag gtg atc tta gtg gag ggc agc aaa cgt ttg gga ggc tgg	268
	26	Pro Pro Lys Val Ile Leu Val Glu Gly Ser Lys Arg Leu Gly Gly Trp	
	27	30 35 40	
W-->	28	atc cgt tca gtc cga gga tca gat ggt gcg atc ttt gaa ctt gga cct	316
	29	Ile Arg Ser Val Arg Gly Ser Asp Gly Ala Ile Phe Glu Leu Gly Pro	
	30	45 50 55	
W-->	31	cga gga att agg' ccg gct gga gcc ctg gga gcc cgg acc ctg ctc ctg	364
	32	Arg Gly Ile Arg Pro Ala Gly Ala Leu Gly Ala Arg Thr Leu Leu Leu	
	33	60 65 70	
W-->	34	gtt tct gaa ctt ggc ttg gaa tcc gaa gtc ttg cct gtc cga ggg gat	412
	35	Val Ser Glu Leu Gly Leu Glu Ser Glu Val Leu Pro Val Arg Gly Asp	
	36	75 80 85 90	
W-->	37	cat cca gct gcc cag aac cgg ttc ctg tat gta ggc ggt gcc ctg cac	460
	38	His Pro Ala Ala Gln Asn Arg Phe Leu Tyr Val Gly Gly Ala Leu His	
	39	95 100 105	

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W-->	40	ccc cta ccc tct ggc ctc agg ggg cta ctt cgt cct tca ccc ccc ttc	508
	41	Pro Leu Pro Ser Gly Leu Arg Gly Leu Leu Arg Pro Ser Pro Pro Phe	
	42	110 115 120	
W-->	43	tca aaa cct cta ttt tgg gct gga ctg agg gag ttg acg aag ccc agg	556
	44	Ser Lys Pro Leu Phe Trp Ala Gly Leu Arg Glu Leu Thr Lys Pro Arg	
	45	125 130 135	
W-->	46	ggc aaa gag cct gat gag act gtg cac agt ttt gcc cag cgc cgc ctt	604
	47	Gly Lys Glu Pro Asp Glu Thr Val His Ser Phe Ala Gln Arg Arg Leu	
	48	140 145 150	
W-->	49	gga cct gag gtg gcg tct ctg gct atg gac agc ctt tgc aga gga gtg	652
	50	Gly Pro Glu Val Ala Ser Leu Ala Met Asp Ser Leu Cys Arg Gly Val	
	51	155 160 165 170	
W-->	52	ttt gct ggc aac agc caa gag ctc agc atc cgg tcc tgc ttt ccc agt	700
	53	Phe Ala Gly Asn Ser Gln Glu Leu Ser Ile Arg Ser Cys Phe Pro Ser	
	54	175 180 185	
W-->	55	ctc ttc caa gct gaa caa acc cac ggg tcc atg tta ctg ggg ctg ctg	748
	56	Leu Phe Gln Ala Glu Gln Thr His Gly Ser Met Leu Leu Gly Leu Leu	
	57	190 195 200	
W-->	58	ctg ggg gca ggg caa act cca cag ccc aat tcc tca tta att cgt cag	796
	59	Leu Gly Ala Gly Gln Thr Pro Gln Pro Asn Ser Ser Leu Ile Arg Gln	
	60	205 210 215	
W-->	61	gcc cgc gct gag cga tgg agt cag tgg tca ctc cgt gga ggg ctg gag	844
	62	Ala Arg Ala Glu Arg Trp Ser Gln Trp Ser Leu Arg Gly Gly Leu Glu	
	63	220 225 230	
W-->	64	atg ttg ccc cag gcc ctt cat aac tac cta aca agt aaa ggg gtc act	892
	65	Met Leu Pro Gln Ala Leu His Asn Tyr Leu Thr Ser Lys Gly Val Thr	
	66	235 240 245 250	
W-->	67	atc ctc agt ggt cag cca gcc tgc ggg ctc agc ctt cag cca gaa ggg	940
	68	Ile Leu Ser Gly Gln Pro Ala Cys Gly Leu Ser Leu Gln Pro Glu Gly	
	69	255 260 265	
W-->	70	cac tgg aag gtg tct cta ggg gac agc agt ctg gag gct gac cac att	988
	71	His Trp Lys Val Ser Leu Gly Asp Ser Ser Leu Glu Ala Asp His Ile	
	72	270 275 280	
W-->	73	ata agc acc att cca gct tca gtg ctc agc aag ctg ctc cct gcc gag	1036
	74	Ile Ser Thr Ile Pro Ala Ser Val Leu Ser Lys Leu Leu Pro Ala Glu	
	75	285 290 295	
W-->	76	gct gca cct ctg gct cac atc ctg agt acc atc caa gct gtg tct gtg	1084
	77	Ala Ala Pro Leu Ala His Ile Leu Ser Thr Ile Gln Ala Val Ser Val	
	78	300 305 310	
W-->	79	gcc gtg gtg aat ctg cag tac aaa gga gct tgt ctg cct gtg cag gga	1132
	80	Ala Val Val Asn Leu Gln Tyr Lys Gly Ala Cys Leu Pro Val Gln Gly	
	81	315 320 325 330	
W-->	82	ttt gga cat ctg gtg cca tcc tca gaa gac ccg acc gtc ctg gga atc	1180
	83	Phe Gly His Leu Val Pro Ser Ser Glu Asp Pro Thr Val Leu Gly Ile	
	84	335 340 345	
W-->	85	gtg tat gac tcg gtt gct ttt cct gag cag gat ggg aac ccc cca ggc	1228
	86	Val Tyr Asp Ser Val Ala Phe Pro Glu Gln Asp Gly Asn Pro Pro Gly	
	87	350 355 360	
W-->	88	ctc aga ctg act gtg atg ttg gga ggt tac tgg tta cag aag ctg aaa	1276
	89	Leu Arg Leu Thr Val Met Leu Gly Gly Tyr Trp Leu Gln Lys Leu Lys	

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90          365          370          375
W--> 91      gcc aat ggc cat gaa ttg tct cca gag cta ttc caa cga gca gca cag      1324
92      Ala Asn Gly His Glu Leu Ser Pro Glu Leu Phe Gln Arg Ala Ala Gln
93          380          385          390
W--> 94      gaa gcg gct gcc aca cag tta gga ctg aaa gag caa cca agc cat tgc      1372
95      Glu Ala Ala Ala Thr Gln Leu Gly Leu Lys Glu Gln Pro Ser His Cys
96      395          400          405          410
W--> 97      ttg gtc cat cta cac aaa aac tgt atc cct cag tat aca cta ggc cac      1420
98      Leu Val His Leu His Lys Asn Cys Ile Pro Gln Tyr Thr Leu Gly His
99          415          420          425
W--> 100     tgg caa aaa cta gac tca gct ctg caa ttc ctg acg gcc cag agg ttg      1468
101     Trp Gln Lys Leu Asp Ser Ala Leu Gln Phe Leu Thr Ala Gln Arg Leu
102          430          435          440
W--> 103     ccc ctg act ttg gct ggg gcc tcc tat gag ggg gta gct gtc aat gac      1516
104     Pro Leu Thr Leu Ala Gly Ala Ser Tyr Glu Gly Val Ala Val Asn Asp
105          445          450          455
W--> 106     tgt ata gag agt ggg cgc cag gca gca att gct gtc ctg ggc aca gaa      1564
107     Cys Ile Glu Ser Gly Arg Gln Ala Ala Ile Ala Val Leu Gly Thr Glu
108          460          465          470
E--> 109     tcg aac agc tga cccccactct cctactcatg aaagtaaaag ttgatggagc      1614
110     Ser Asn Ser
111          475
W--> 112     ttgaaaaaaaa aaaaaaaaaa aa      1636

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113 <210> 14

114 <211> 32

115 <212> DNA

116 <213> Artificial Sequence

117 <220>

118 <223> Designed oligonucleotide primer used for constructing a vector for expressing

119 <400> 14

W--> 120 ttgtcgacta ctacacatcc cagcaagcgc ca

32

E--> 121

122

Input Set: I289180.RAW

Line	? Error/Warning	Original Text
16	E Sequence IDs 1 and 2 differ	<400> 1
17	W Line data has been corrected	CGTACACGCG CGTTTTGCAT TAGTTGCTCA TTAATCAG
18	W Line data has been corrected	GGGACCCGTG GGGTTTCTGC AGTTGTAAAG CAGGGTGC
19	W Line data has been corrected	CGACTTTCCC CCAGGCCTTA CG ATG GCC CGG ACT
22	W Line data has been corrected	GGT ATC AGC GGA TTG GCC GCA AGT TAT CAT C
25	W Line data has been corrected	CCT CCT AAG GTG ATC TTA GTG GAG GGC AGC A
28	W Line data has been corrected	ATC CGT TCA GTC CGA GGA TCA GAT GGT GCG A
31	W Line data has been corrected	CGA GGA ATT AGG CCG GCT GGA GCC CTG GGA G
34	W Line data has been corrected	GTT TCT GAA CTT GGC TTG GAA TCC GAA GTC T
37	W Line data has been corrected	CAT CCA GCT GCC CAG AAC CGG TTC CTG TAT G
40	W Line data has been corrected	CCC CTA CCC TCT GGC CTC AGG GGG CTA CTT C
43	W Line data has been corrected	TCA AAA CCT CTA TTT TGG GCT GGA CTG AGG G
46	W Line data has been corrected	GGC AAA GAG CCT GAT GAG ACT GTG CAC AGT T
49	W Line data has been corrected	GGA CCT GAG GTG GCG TCT CTG GCT ATG GAC A
52	W Line data has been corrected	TTT GCT GGC AAC AGC CAA GAG CTC AGC ATC C
55	W Line data has been corrected	CTC TTC CAA GCT GAA CAA ACC CAC GGG TCC A
58	W Line data has been corrected	CTG GGG GCA GGG CAA ACT CCA CAG CCC AAT T
61	W Line data has been corrected	GCC CGC GCT GAG CGA TGG AGT CAG TGG TCA C
64	W Line data has been corrected	ATG TTG CCC CAG GCC CTT CAT AAC TAC CTA A
67	W Line data has been corrected	ATC CTC AGT GGT CAG CCA GCC TGC GGG CTC A
70	W Line data has been corrected	CAC TGG AAG GTG TCT CTA GGG GAC AGC AGT C
73	W Line data has been corrected	ATA AGC ACC ATT CCA GCT TCA GTG CTC AGC A
76	W Line data has been corrected	GCT GCA CCT CTG GCT CAC ATC CTG AGT ACC A
79	W Line data has been corrected	GCC GTG GTG AAT CTG CAG TAC AAA GGA GCT T
82	W Line data has been corrected	TTT GGA CAT CTG GTG CCA TCC TCA GAA GAC C
85	W Line data has been corrected	GTG TAT GAC TCG GTT GCT TTT CCT GAG CAG G
88	W Line data has been corrected	CTC AGA CTG ACT GTG ATG TTG GGA GGT TAC T
91	W Line data has been corrected	GCC AAT GGC CAT GAA TTG TCT CCA GAG CTA T
94	W Line data has been corrected	GAA GCG GCT GCC ACA CAG TTA GGA CTG AAA G
97	W Line data has been corrected	TTG GTC CAT CTA CAC AAA AAC TGT ATC CCT C
100	W Line data has been corrected	TGG CAA AAA CTA GAC TCA GCT CTG CAA TTC C
103	W Line data has been corrected	CCC CTG ACT TTG GCT GGG GCC TCC TAT GAG G
106	W Line data has been corrected	TGT ATA GAG AGT GGG CGC CAG GCA GCA ATT G
109	E Number of Bases conflict w/ Running Total	TCG AAC AGC TGA CCCCCACTCT CCTACTCATG AAA
112	W Line data has been corrected	TTGAAAAAAA AAAAAAAAAA AA
120	W Line data has been corrected	TTGTCGACTA CTACACATCC CAGCAAGCGC CA
121	E Number of Bases conflict w/ Running Total	1

Input Set: I289180.RAW

Line	Original Text	Corrected Data
17	CGTACACGCG CGTTTTGTCAT TAGTTGCTCA TTAATCAG	cgtacacgcg cgttttgcata tagttgctca ttaatcag
18	GGGACCCGTG GGGTTTCTGC AGTTGTAAAG CAGGGTGC	gggaccgtg gggtttctgc agttgtaaag caggggtgc
19	CGACTTTCCC CCAGGCCTTA CG ATG GCC CGG ACT	cgactttccc ccaggcctta cg atg gcc cgg act
22	GGT ATC AGC GGA TTG GCC GCA AGT TAT CAT C	ggt atc agc gga ttg gcc gca agt tat cat c
25	CCT CCT AAG GTG ATC TTA GTG GAG GGC AGC A	cct cct aag gtg atc tta gtg gag ggc agc a
28	ATC CGT TCA GTC CGA GGA TCA GAT GGT GCG A	atc cgt tca gtc cga gga tca gat ggt gcg a
31	CGA GGA ATT AGG CCG GCT GGA GCC CTG GGA G	cga gga att agg ccg gct gga gcc ctg gga g
34	GTT TCT GAA CTT GGC TTG GAA TCC GAA GTC T	gtt tct gaa ctt ggc ttg gaa tcc gaa gtc t
37	CAT CCA GCT GCC CAG AAC CGG TTC CTG TAT G	cat cca gct gcc cag aac cgg ttc ctg tat g
40	CCC CTA CCC TCT GGC CTC AGG GGG CTA CTT C	ccc cta ccc tct ggc ctc agg ggg cta ctt c
43	TCA AAA CCT CTA TTT TGG GCT GGA CTG AGG G	tca aaa cct cta ttt tgg gct gga ctg agg g
46	GGC AAA GAG CCT GAT GAG ACT GTG CAC AGT T	ggc aaa gag cct gat gag act gtg cac agt t
49	GGA CCT GAG GTG GCG TCT CTG GCT ATG GAC A	gga cct gag gtg gcg tct ctg gct atg gac a
52	TTT GCT GGC AAC AGC CAA GAG CTC AGC ATC C	ttt gct ggc aac agc caa gag ctc agc atc c
55	CTC TTC CAA GCT GAA CAA ACC CAC GGG TCC A	ctc ttc caa gct gaa caa acc cac ggg tcc a
58	CTG GGG GCA GGG CAA ACT CCA CAG CCC AAT T	ctg ggg gca ggg caa act cca cag ccc aat t
61	GCC CGC GCT GAG CGA TGG AGT CAG TGG TCA C	gcc cgc gct gag cga tgg agt cag tgg tca c
64	ATG TTG CCC CAG GCC CTT CAT AAC TAC CTA A	atg ttg ccc cag gcc ctt cat aac tac cta a
67	ATC CTC AGT GGT CAG CCA GCC TGC GGG CTC A	atc ctc agt ggt cag cca gcc tgc ggg ctc a
70	CAC TGG AAG GTG TCT CTA GGG GAC AGC AGT C	cac tgg aag gtg tct cta ggg gac agc agt c
73	ATA AGC ACC ATT CCA GCT TCA GTG CTC AGC A	ata agc acc att cca gct tca gtg ctc agc a
76	GCT GCA CCT CTG GCT CAC ATC CTG AGT ACC A	gct gca cct ctg gct cac atc ctg agt acc a
79	GCC GTG GTG AAT CTG CAG TAC AAA GGA GCT T	gcc gtg gtg aat ctg cag tac aaa gga gct t
82	TTT GGA CAT CTG GTG CCA TCC TCA GAA GAC C	ttt gga cat ctg gtg cca tcc tca gaa gac c
85	GTG TAT GAC TCG GTT GCT TTT CCT GAG CAG G	gtg tat gac tcg gtt gct ttt cct gag cag g
88	CTC AGA CTG ACT GTG ATG TTG GGA GGT TAC T	ctc aga ctg act gtg atg ttg gga ggt tac t
91	GCC AAT GGC CAT GAA TTG TCT CCA GAG CTA T	gcc aat ggc cat gaa ttg tct cca gag cta t
94	GAA GCG GCT GCC ACA CAG TTA GGA CTG AAA G	gaa gcg gct gcc aca cag tta gga ctg aaa g
97	TTG GTC CAT CTA CAC AAA AAC TGT ATC CCT C	ttg gtc cat cta cac aaa aac tgt atc cct c
100	TGG CAA AAA CTA GAC TCA GCT CTG CAA TTC C	tgg caa aaa cta gac tca gct ctg caa ttc c
103	CCC CTG ACT TTG GCT GGG GCC TCC TAT GAG G	ccc ctg act ttg gct ggg gcc tcc tat gag g
106	TGT ATA GAG AGT GGG CGC CAG GCA GCA ATT G	tgt ata gag agt ggg cgc cag gca gca att g
109	TCG AAC AGC TGA CCCCCACTCT CCTACTCATG AAA	tcg aac agc tga cccccactct cctactcatg aaa
112	TTGAAAAAAA AAAAAAAAAA AA	ttgaaaaaaaa aaaaaaaaaa aa
120	TTGTCGACTA CTACACATCC CAGCAAGCGC CA	ttgtcgacta ctacacatcc cagcaagcgc ca